```
                -29          5'UTR          -1+1  M   D   L   V   L   R   K   Y   L   L      10
GGTCTTTGGTTGCTGGAAGGAAGAACAGG ATG GAT CTG GTG CTG AGA AAA TAC CTT CTC      30
SIL5 ---------->

  H   V   A   L   M   G   V   L   L   A   V   R   T   T   E   G   P   R      28
CAT GTG GCT CTG ATG GGT GTT CTT CTG GCT GTA AGG ACC ACA GAA GGA CCC AGA      84

  D   R   D   W   L   G   V   S   R   Q   L   R   I   K   A   W   N   R      46
GAC AGG GAC TGG CTT GGT GTC TCA AGG CAG CTC AGA ATT AAA GCA TGG AAC AGA     138

  Q   L   Y   P   E   W   T   E   S   Q   G   P   D   C   W   R   G   G      64
CAG CTG TAT CCA GAG TGG ACA GAA AGC CAG GGG CCT GAC TGC TGG AGA GGT GGC     192

  H   I   S   L   K   V   S   N   D   G   P   T   L   I   G   A   N   A      82
CAC ATA TCC CTG AAG GTC AGC AAT GAT GGG CCT ACA CTG ATT GGG GCA AAT GCT     246
                  <---------- SIL2

  S   F   S   I   A   L   H   F   P   K   S   Q   K   V   L   P   D   G     100
TCC TTC TCT ATT GCC TTG CAC TTT CCT AAA AGC CAA AAG GTG CTG CCA GAT GGG     300

  Q   V   I   W   A   N   N   T   I   I   N   G   S   Q   V   W   G   G     118
CAG GTC ATC TGG GCC AAC AAC ACC ATC ATC AAT GGG AGC CAG GTG TGG GGA GGA     354
                  <---------- SIL1

  Q   L   V   Y   P   Q   E   P   D   D   T   C   I   F   P   D   G   E     136
CAG CTG GTA TAT CCC CAA GAA CCT GAT GAT ACC TGC ATC TTC CCC GAT GGG GAG     408

  P   C   P   S   G   P   L   S   Q   K   R   C   F   V   Y   V   W   K     154
CCC TGC CCT TCT GGC CCT CTA TCT CAG AAA AGA TGC TTT GTT TAT GTC TGG AAG     462

  T   W   D   Q   Y   W   Q   V   L   G   G   P   V   S   G   L   S   I     172
ACC TGG GAC CAA TAC TGG CAA GTT CTG GGG GGC CCA GTG TCT GGA CTG AGC ATC     516

  G   T   D   K   A   M   L   G   T   Y   N   M   E   V   T   V   Y   H     190
GGG ACA GAC AAG GCA ATG CTG GGC ACA TAT AAC ATG GAA GTG ACT GTC TAC CAC     570

  R   R   G   S   Q   S   Y   V   P   L   A   H   S   S   S   A   F   T     208
CGC CGG GGG TCC CAG AGC TAT GTG CCC CTC GCT CAC TCC AGT TCA GCC TTC ACC     624

  I   T   D   Q   V   P   F   S   V   S   V   S   Q   L   Q   A   L   D     226
ATT ACT GAC CAG GTG CCC TTC TCT GTG AGT GTG TCT CAG CTG CAG GCC TTG GAT     678

  G   R   N   K   R   F   L   R   K   Q   P   L   T   F   A   L   Q   L     244
GGA AGG AAC AAG CGC TTC CTG AGA AAG CAG CCT CTG ACC TTT GCC CTC CAG CTC     732

  H   D   P   S   G   Y   L   A   G   A   D   L   S   Y   T   W   D   F     262
CAT GAT CCC AGT GGC TAT TTG GCT GGG GCT GAC CTT TCC TAC ACC TGG GAC TTT     786

  G   D   S   T   G   T   L   I   S   R   A   L   T   V   T   H   T   Y     280
GGT GAC AGT ACA GGG ACC CTG ATC TCT CGG GCA CTC ACG GTC ACT CAC ACT TAC     840

  L   E   S   G   P   V   T   A   Q   V   V   L   Q   A   A   I   P   L     298
CTA GAG TCT GGC CCA GTC ACT GCA CAG GTG GTG CTG CAG GCT GCC ATT CCT CTC     894

  T   S   C   G   S   S   P   V   P   G   T   T   D   R   H   V   T   T     316
ACC TCC TGT GGC TCC TCT CCA GTT CCA GGC ACT ACA GAT AGG CAT GTG ACA ACT     948

  A   E   A   P   G   T   T   A   G   Q   V   P   T   T   E   V   M   G     334
GCA GAG GCT CCT GGA ACC ACA GCT GGC CAA GTG CCT ACT ACA GAA GTC ATG GGC    1002

  T   T   P   G   Q   V   P   T   A   E   A   P   G   T   T   V   G   W     352
ACC ACA CCT GGC CAG GTG CCA ACT GCA GAG GCC CCT GGC ACC ACA GTT GGG TGG    1056

  V   P   T   T   E   D   V   G   T   T   P   E   Q   V   A   T   S   K     370
GTG CCA ACC ACA GAG GAT GTA GGT ACC ACA CCT GAG CAG GTG GCA ACC TCC AAA    1110

  V   L   S   T   T   P   V   E   M   P   T   A   K   A   T   G   R   T     388
GTC TTA AGT ACA ACA CCA GTG GAG ATG CCA ACT GCA AAA GCT ACA GGT AGG ACA    1164
```

Figure 1

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 P   E   V   S   T   T   E   P   S   G   T   T   V   T   Q   G   T   T      406
CCT GAA GTG TCA ACT ACA GAG CCC TCT GGA ACC ACA GTT ACA CAG GGA ACA ACT    1218

 P   E   L   V   E   T   T   A   G   E   V   S   T   P   E   P   A   G      424
CCA GAG CTG GTG GAG ACC ACA GCT GGA GAG GTG TCC ACT CCT GAG CCT GCG GGT    1272

 S   N   T   S   S   F   M   P   T   E   G   T   A   G   S   L   S   P      442
TCA AAT ACT AGC TCA TTC ATG CCT ACA GAA GGT ACT GCA GGC TCC CTG AGT CCC    1326

 L   P   D   D   T   A   T   L   V   L   E   K   R   Q   A   P   L   D      460
CTG CCG GAT GAC ACT GCC ACC TTA GTC CTG GAG AAG CGC CAA GCC CCC CTG GAT    1380

 C   V   L   Y   R   Y   G   S   F   S   L   T   L   D   I   V   Q   G      478
TGT GTT CTG TAT CGC TAT GGC TCC TTT TCC CTC ACC CTG GAC ATT GTC CAG GGT    1434

 I   E   S   A   E   I   L   Q   A   V   S   S   S   E   G   D   A   F      496
ATT GAG AGT GCT GAG ATC CTA CAG GCT GTG TCA TCC AGT GAA GGA GAT GCA TTT    1488

 E   L   T   V   S   C   Q   G   G   L   P   K   E   A   C   M   D   I      514
GAG CTG ACT GTG TCT TGC CAA GGC GGG CTA CCC AAG GAA GCC TGC ATG GAC ATC    1542

 S   S   P   G   C   Q   L   P   A   Q   R   L   C   Q   P   V   P   P      532
TCA TCG CCA GGG TGT CAG CTG CCT GCC CAG CGG CTG TGT CAG CCT GTG CCC CCC    1596

 S   P   A   C   Q   L   V   L   H   Q   V   L   K   G   G   S   G   T      550
AGC CCA GCC TGC CAG CTG GTT TTG CAC CAG GTA CTG AAG GGT GGC TCA GGG ACC    1650

 Y   C   L   N   V   S   L   A   D   A   N   S   L   A   M   V   S   T      568
TAC TGC CTC AAT GTG TCT TTG GCT GAT GCC AAT AGC CTG GCG ATG GTC AGC ACC    1704
SIL3 ------------------------------>
 Q   L   V   M   P   G   Q   E   A   G   L   R   Q   A   P   L   F   V      586
CAG CTT GTC ATG CCT GGG CAA GAA GCA GGC CTC AGG CAG GCT CCT CTG TTC GTG    1758

 G   I   L   L   V   L   T   A   L   L   L   A   S   L   I   Y   R   R      604
GGC ATC TTG CTG GTG CTA ACA GCT TTG TTG CTT GCA TCT CTG ATA TAC AGG CGA    1812

 R   L   M   K   Q   G   S   A   V   P   L   P   Q   L   P   H   G   R      622
AGA CTT ATG AAG CAA GGC TCA GCA GTC CCC CTT CCC CAG CTG CCA CAC GGT AGA    1866

 T   Q   W   L   R   L   P   W   V   F   R   S   C   P   I   G   E   S      640
ACC CAG TGG CTA CGT CTG CCC TGG GTC TTC CGC TCT TGC CCC ATT GGT GAG AGC    1920

 K   P   L   L   S   G   Q   Q   V   *                                  SIL7 649
AAA CCC CTC CTC AGT GGA CAG CAG GTC TGA GTG CTC TTA TGT GAA GTC ATG ATT    1974
SIL4 ------------------------------>
TAC CCA GGT GGA CAG CAA GGC CTG TCT TTT CTC TGG TCT TCC CTC AGA GAC TAC    2028
                    <------------------------------ SIL6
CAT TGC CTG AAA TAA AGA CTC AGA ACT TG          Poly(A)                    2057
                    <------------------------------ SIL9
                    3'UTR
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Figure 1 (continued)

SIL10 →

GTTGCTGGAAGGAAGAACAGGATGGATCTGGTGCTGAGAAAATACCTTCTCCATGTGGCTCTGATGGGTGTTCTTCTGGC 80

TGTAAGGACCACAGAAGGTGAGTGTGGGATGTTGGACATGAACAAGTGTGAATTTGGGGTTGCACACCTGCTCTGGTTTT 160

TCTCTCCCTAAAATGGAAGATATCAGTAGTGCTTCAGGTGTCTCCCACCCATTTGATTTAGTGAGGACATGGGCAACTGA 240

GCTCCCTCCCCACATGAAGATTTGGGTGCATGTGTGTTCAGGCACTTGGGACTGAACCTGAAAACAACCCCATCTACCTG 320

← SIL8

GATGGGTGAGAGAACAGTATGTCTCCGTGGCCCTAATTTTGAGATGCTCTGAATAGTGAGCTGGAACATGGGTGCCAAGG 400

TAGTAAAATGAGTGGAAACTCATTTAGGCTTTGTCTCAGGCACTTGGGATAGGGTATTTAGGAGATAGAGAAAGATAGGA 480

GATAGGAGAAAGGAGAAAGAGGATGTGGTATTGGATAGAAGGGTAATGAGGCACCTCATCCCCTCTTTGGGATGGGCATG 560

GGTGAACACAGCCCAGGCTTTTGTTCTGGGGCTGGAAGAGACAGGCAGAAGGGTCTCAGCTGAGCATCACATGAAAGGGC 640

TCTGGGGGATTGGGGCCTCGTGACAGGAGCAAGGCGGGTGGGGTGGGGATGGTGAGAGGGTCTGGAATGTCCCGTGCTGC 720

TCTGAGGAGGGAGGATTGGGAGTGGAGAAAGAATGGGGCATCTTATGATTCTCTTGTTCTTGTGGTGAGGTATTCAGTGG 800

GATAATTCTAGATCCTCCCCCAAGAGAATCAACCAGGTTTCTGGTACATGTTAGAGATGGAGTGAGGATAGTCTGTGATG 880

TGCAGAAATATCTACATTGTACCCCAGTGCCCCCTTTCTCTAGATCCCTGGTCTCACAGACTTCTTGGAACTTCTCCTTG 960

ATCTGACTTCCCTCATTCATGGTGTCATTTCAAGTCTTATTCTTTTACTATGTTCGTTATTGTATTCTGGAAATATCCTG 1040

TTCATATGTGTCCACCCAAGGCTCTTAATATGTTGTGCTTACTTTTTGGATCCAGATTTTTAAAATCATAAGAAGACATT 1120

TTTATATAGTTCATGAAATTTTGCATGGACTGAGTTTGATAATTTTGTTTAGTGTGAATTAACATTGTGTTTATTTAAGA 1200

AAAAAAAATATTTTTTTACAGAAACCTACTGAATTTGTAGGGTTTTAAAATAACATGATGTCTGGGATTTGCTTTTGAAT 1280

GCTTCAGCCAAAAAACAAACGAACAACAAAAATAAAGGATAGATAAAGCAAATGTGACAAAATGCTGATAGTTGTTGGAC 1360

CTTGGGGAGACACATGCAGAGCCATCACATCACTTTTTTTCAGACATCTTTCTTGGTCAGTTATAATCATTTTGTTTGTC 1440

CCCACTCCCAATTTCTACTTGCCTCTAGTCCATCCTCCTCACTGCTTGCCAAAGTGATCCTTCTAAAACACAAATCTGAT 1520

CATATTCAAAAAGCTTTTGAAGGGTAAGTTTTATGGTATATGCCATATATCAGTACAACAAACAAAATCGTCTGAGGTGC 1600

CGTTGCCTACAGGATAAAGTCCAAACTCCTTTGCCTGGCACTCCAAGCCCCCACTCTATCTTCTTGGCCTCATCTCTCAT 1680

GATGTACATCAGCCACATTGCTAGTGTCTGCTCATGGCCTTCTGCCTAGAATGCTTTATGCCCCAGCCAACTATTTACTG 1760

TCTTCTTCAGTCGACCAGAGTGCAATTTACCTGTTTAAAATCTATCATTTTGTTATACATTGTGCATGTCTATTATGGCT 1840

CATATTAAGCAATGCCTTGGATTATAGTAATTTATGTATATGTCTATTTCATATACTTTAACCTGAACCCCTTCAGAACC 1920

ATTTCTTTTTCATTTCTTAAGTTCTTTGCACCTAGCCCAGTGCCTGGTACGTCGTGGGTATTCAGTAGATTAAAATGCAC 2000

TTTAAGGAACTTCCCTTGTTGTCCATCAAGTGGCTAAGGCTCTGTGCTCCCAATGCAGGGGACCAGGGTTCAATCTCAGG 2080

TCAGGGAACTAGATCCCACAGGTCACAACTAAGAGTTTGCAAGCCACAACTACCTGACCTCACATGCCACAACTAATCGA 2160

AGATCCCTCGTGCTGCAACTAAGTCCTAGTGCAGTTAAATATATTTTTTTAATGCACTTTGAATGTGAGAATGAATGATG 2240

TGTCACAGACACTGTTGTCCCCTGAGAAGGGAGTGAGTAATGATTTGAGGGCCCTCATAGTATATCTTCCTTTTTAGGAC 2320

CCAGAGACAGGGACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAAGCATGGAACAGACAGCTGTATCCAGAGTGGACA 2400

GAAAGCCAGGGGCCTGACTGCTGGAGAGGTAGGAACTTGGCAATTTCCAGGGAGGATATGGTGGAAATGGGTGGGGAGGG 2480

GAACGGGGTTGAATGTACTTAGGAAGATAGGGAAGGAAAAGGCATACAGGGAGGAGAAGCCAAGGAGCTAATTAATGCAG 2560

CTGCCCTTTTCAGGTGGCCACATATCCCTGAAGGTCAGCAATGATGGGCCTACACTGATTGGGGCAAATGCTTCCTTCTC 2640

TATTGCCTTGCACTTTCCTAAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCATCTGGGCCAACAACACCATCATCAATG 2720

GTGAGTACCTCTCCGCCTCCTTCCCAAGGTCCAGAATCCCTGGTATCCCCAATGAGCTCAAGGAATCCTCCTCCTCTTTT 2800

TTTTTTTTTTTTTTTACAAATTATATATGTAACACATATTCACTGCAGAAAAATTAGAAAACACAGATAAACCAAAAAGA 2880

Figure 2

AAAAAAATTATAGTTCCCCAAATGGGGCACAGAAGACCCAGTGGACATAGAAGTTGGATAGACTTGGATTTAAACTGGTT 2960

ACCAGTATGTGACCCTGGACAAGTCACTGAATTGTTTTGTTCTTCCATTCCCTTATCTATAGAATGGGGATGATAACACT 3040

TTAAAAGGTTCTTGTAAGGATTAAAATGTGATAATATATAAAGATTTTAGCATAATGCCTGCCCTGTGCTGTGCTTAGTA 3120

CCTTAGTTTAGACGCTTTGCAACCCCATGGACTGTAGCCCACCAGGCTCCTCTGTCCATGTGGATTCTGCAGGCAAGAAT 3200

ACTGGAGTGGGTCACCATGCACTCCTCCAGGGGATCTTCCCAACTCAGGGATCGAACCCAGGTCCTAGCCTACAGTATTA 3280

ATTGATGCTGTTATTTTTACTTTTATCCCACTAGCTAGAGCACATCATCCTAGACATTTTGATACATGGCCTACCAATTT 3360

GTGTCCAGTGTAAGAATATACATGTGTGTGCTCAGTGGCTCAGTCGTGTCTGACTCTTTGCAACCCCATGGACTGTAGCC 3440

CGCGAAAGCTCCTCTGCCCATGGGATTGCCCAGCCAAGAATACTGGAGCAGGTTGCCATTTCTTCCTCCAGGGGATCTTT 3520

CAACACAGGGATTGAATCCTTGTCTCCTGTGTTTCCTGCATTGGCAGGTGTATTCTTTACCACTGAGCCACCTGGGAAAC 3600

CCCTTAAGTATATACACATAAATCTTTTATAGTTTCCATTCTCCCTTCTACCACTCCAAATAGGTTATACCAAGGAGAAT 3680

GTATTTTGGTAGCTAGGCAGTATTCCTGGAGCCCCTCTCTGGGAGTCATGTTAAAGGTTTTGGTGTACAGTGAGGAATGC 3760

CAGGGATTGAGGGAGACTTGCTGTCTTCTTTTCAGGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTG 3840

ATGATACCTGCATCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTTATGTCTGG 3920

AAGACCTGGGGTAAGAGTTTCCCTTCTCTGGCCTGTCATTCACACTTAAATTCACTTCTTCCTACCTGATCCCCTTTCTT 4000

TTGGTCTCATCCTTAAATTCTGTGAGTTTCCCTAATCTTCACTTCCCCCATGACTCCTTCCTCTTCCACAGCACCTAGTC 4080

AACTCTATTATACTTCTTTCTGGGAGCCCTGCTCCAATTATAGTCCCATCCCATGGACCCTCTCATAAGGACTTTTTTCC 4160

TGCCCAACATATGCAAGCTTAAACTCTCTGAAATAACCATCCTTGATACATCTCCTGACCTTCCTTCTCTGGTTCCATCT 4240

CTAACCCTGCCCCAGTCTCCTTTGACCAGTAACCCCCTTCCCTACTCTTCTTTCCAAAAACCTCAGACCAATACTGGCAA 4320

GTTCTGGGGGGCCCAGTGTCTGGACTGAGCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGT 4400

CTACCACCGCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTGGTAAGGACTGAG 4480

GAGGGGACAAGGCCAGTTGCAGGGCAGGAGAAGGTGGGGAGGCTGGGCTGGACAGGAAAGGGGAAAGAGGAAATGGTGTG 4560

TAACCTTACAGGGGCAGAACCAGGAAGATGTGGGCAGAGGGATGTGGGGCTTGGAGCCCGTGAAGGGCCAGGCAGCTTGG 4640

GTTGGTTGAAAAATATGGCTGTGAAAGAAGAAGCTGACAGAAAGAAGAACTTATGGTTCTCACTTTCTCTGACTCCAATC 4720

CCAGACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGCGCTTCCTGAGAAAGCA 4800

GCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATTTGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTG 4880

GTGACAGTACAGGGACCCTGATCTCTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAG 4960

GTGGTGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAGATAGGCATGTGACAAC 5040

TGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAGAAGTCATGGGCACCACACCTGGCCAGGTGCCAACTG 5120

CAGAGGCCCCTGGCACCACAGTTGGGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCC 5200

AAAGTCTTAAGTACAACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAGTGTCAACTACAGAGCC 5280

CTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGGAGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTG 5360

CGGGTTCAAATACTAGCTCATTCATGCCTACAGAAGGTACTGCAGGTAAGGGGGCCACCATGAATGAGTTCATAGAGGTG 5440

GGGCATTTGTCACAGCTCTGAAGACCTGAAAGAATTGCTCAGGACCCAGATGTTACTCAATCCTTAGCTTAGCAGTGGAG 5520

TCCCCTCAGAATCTTCACTGGTTTTAAAACCCCCTAAGTCCCTCTTAATGGCACAGAATAGATCCAGAGTTCAGGAAACC 5600

AGGGTCTTCTCCTAGGCCAGGGGTAGAGAGCTTATTCTCTCTTCCTGAAGAGAAGTTCAGGAAGCAGTGTGTGATCATTT 5680

GGTGGTGGTGCTCAGTCATGTCTGACTCTTTGTGACCTCATGGACTATGGCCCACCAGGCTCCTCTGTCCATAGAATTCT 5760

Figure 2 (continued 1)

CCAGGCAAGAACACTGGAGTGGGTGGCCATTTCCTTCTCCAGGGGATTTTCCCTGCCCAGGGATTAAACCCGAATTGGCA 5840

GGTGGATTCTTTACCCGAGCCACCTAGAAAGTCCCATGTGATCATTAGATAATACTTATACCTCATTTTCTGATTAAGTG 5920

TAAACACAGAAATCTTTCTGACACCACTTCCCACCCCTGGATTCCCATCCCAAAGTAGGTTTACCTGGAATTGTGGTAGG 6000

AATACTAAAAAGGGAGAAGTGAGATAGTGACACTATGACTTAACACATGTCAAATGTCTGACCCAGGACCTGGCACAGTG 6080

TAGGGTGTGATAAACATTTGGGATGTCTAAAATTCTGACTCTAACCCTGTGACTCTGGGGCAGTCATTTCTCTTGGGCCT 6160

TTCTTTATCTTAAAAAATGAGAGTTTCCAGCTCTTGTCTGATTCTAAGCCTGGATCCAGTAGCTCTGACTCTACCTGGAA 6240

AAATGCTTGTTGGGCCTGTTTTCAGGTTAGTCATTTGCTTTTTGACTTTGCCTCTTTAATCCTCTCCTCCAGGCTCCCTG 6320

AGTCCCCTGCCGGATGACACTGCCACCTTAGTCCTGGAGAAGCGCCAAGCCCCCCTGGATTGTGTTCTGTATCGCTATGG 6400

CTCCTTTTCCCTCACCCTGGACATTGTCCGTGAGTCTTGCCTACATTGTCCGTAAGCTGGTGGAGGGAGGCGTGTGCTGC 6480

TTAGGGTTGCCCAGTGGAAGCACACCTTGGAAGGAATTACTCACCTGGACAAGGAGAATACCCAGATCCCAGGGGTTTCA 6560

TATGAAGGCAGAATGGGATTAGGGAGGCAGCCCGAGGACCTTCCTGGCCATGGGCCTTGGGGGAGGATAAGTAGAGGAGT 6640

CTCAGACTTAAAAAAATCTTGCAACTTTGCAGAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCAGTGAAG 6720

GAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGTGAGTGTCCCACGGTTGCCCTGAGAACTCCTGGGGTGACTGC 6800

TGTCCTGTTCTCTGGTGTCTAGTGTCCCTTCCCAGATTCCCTGACGTAAGCTGACATCTCTCCCAGGCTACCCAAGGAAG 6880

CCTGCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGCCCCCCAGCCCAGCCTGC 6960

CAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCTACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCT 7040

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GGTTACCTACTAGAGGAAGCAGACACTGAATGCAGCCGTATCTGGGATTCCACCCATAGGGCAAGAAGCAGGCCTCAGGC 7200

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CATCCTGCTCCCACTCCTTTACCCCTTATTACCACCACCACTCTTCCTCATGGGAAGAAGAAACCACCAACCCCTTTGGG 7360

AAAGTGTAGAGTCCAAGAAAGAGCCCAGACTTGGAAGTTCAACAGGTCTAGGCTGCAGTCTTGCTGGTGGGACCCTGGGG 7440

AAGTCCATTAACCCTTCTGAGCCACTGAAAAGTAGGAAACATAATACCTGTCCTGTGGGGCTGTTTTCAGGGCTCTAGAC 7520

AATGTGAGTAAAACACCTGGTTCTGAAACAAAAGTGGAATAAATGATGATCTCAATGACTGTTGTTATGAATAATATCAA 7600

CAGTGGAGAAGAACTCAGTGAACTGAGTTCTCCACCTGCCAGAAAGGCAAATCCCTAGGCCTGGAGGGCTGAGGTCCTCA 7680

AAGCAGGGAAGCCTGTAGGGTGAGAGGGAAATGGTCAGAGCTTACCATAAACATAAGAGAGGATAAACCCTGTTGGTGAG 7760

AAGAGGAGGGAGCCAGGATCAAGACCAAGTCAACCTGGGTTATGGTTTAGTCTTTTTTTTTTAGAGAAGCACAAAGAGGT 7840

TGCCATTGACCACCACTAACCAGTATCCCTGCTTTTCTCCCAATATCAGGCGAAGACTTATGAAGCAAGGCTCAGCAGTC 7920

CCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGGTCTTCCGCTCTTGCCCCATTGGTGAGAG 8000

CAAACCCCTCCTCAGTGGACAGCAGGTCTGAGTGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGT 8080

CTTTTCTCTGGTCTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 8138

SIL9

Figure 2 (continued 2)

```
cDNA CH      GGTCTTTGGTTGCTGGAAGGAAGAACAGGATGGATCTGGTGCTGAGAAAATACCTTCTCC 60
cDNA RPE1    ------------------------------------------------------------

cDNA CH      ATGTGGCTCTGATGGGTGTTCTTCTGGCTGTAAGGACCACAGAAGGACCCAGAGACAGGG 120
cDNA RPE1    ------------------------------------------------------------

cDNA CH      ACTGGCTTGGTGTCTCAAGGCAGCTCAGAATTAAAGCATGGAACAGACAGCTGTATCCAG 180
cDNA RPE1    ------------------------------------------------------------

cDNA CH      AGTGGACAGAAAGCCAGGGGCCTGACTGCTGGAGAGGTGGCCACATATCCCTGAAGGTCA 240
cDNA RPE1    ------------------------------------------------------------

cDNA CH      GCAATGATGGGCCTACACTGATTGGGGCAAATGCTTCCTTCTCTATTGCCTTGCACTTTC 300
cDNA RPE1    ------------------------------------------------------------

cDNA CH      CTAAAAGCCAAAAGGTGCTGCCAGATGGGCAGGTCATCTGGGCCAACAACACCATCATCA 360
cDNA RPE1    ------------------------------------------------------------

cDNA CH      ATGGGAGCCAGGTGTGGGGAGGACAGCTGGTATATCCCCAAGAACCTGATGATACCTGCA 420
cDNA RPE1    ------------------------------------------------------------

cDNA CH      TCTTCCCCGATGGGGAGCCCTGCCCTTCTGGCCCTCTATCTCAGAAAAGATGCTTTGTTT 480
cDNA RPE1    ------------------------------------------------------------

cDNA CH      ATGTCTGGAAGACCTGGGACCAATACTGGCAAGTTCTGGGGGGCCCAGTGTCTGGACTGA 540
cDNA RPE1    --------------------CCAATACTGGCAAGTTCTGGGGGGCCCAGTGTCTGGACTGA 41
                                 ****************************************

cDNA CH      GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC 600
cDNA RPE1    GCATCGGGACAGACAAGGCAATGCTGGGCACATATAACATGGAAGTGACTGTCTACCACC 101
             ************************************************************

cDNA CH      GCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG 660
cDNA RPE1    GCCGGGGGTCCCAGAGCTATGTGCCCCTCGCTCACTCCAGTTCAGCCTTCACCATTACTG 161
             ************************************************************

cDNA CH      ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC 720
cDNA RPE1    ACCAGGTGCCCTTCTCTGTGAGTGTGTCTCAGCTGCAGGCCTTGGATGGAAGGAACAAGC 221
             ************************************************************

cDNA CH      GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT 780
cDNA RPE1    GCTTCCTGAGAAAGCAGCCTCTGACCTTTGCCCTCCAGCTCCATGATCCCAGTGGCTATT 281
             ************************************************************

cDNA CH      TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT 840
cDNA RPE1    TGGCTGGGGCTGACCTTTCCTACACCTGGGACTTTGGTGACAGTACAGGGACCCTGATCT 341
             ************************************************************

cDNA CH      CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG 900
cDNA RPE1    CTCGGGCACTCACGGTCACTCACACTTACCTAGAGTCTGGCCCAGTCACTGCACAGGTGG 401
             ************************************************************

cDNA CH      TGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAG 960
cDNA RPE1    TGCTGCAGGCTGCCATTCCTCTCACCTCCTGTGGCTCCTCTCCAGTTCCAGGCACTACAG 461
             ************************************************************
```

Figure 3

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cDNA CH         ATAGGCATGTGACAACTGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAG 1020
cDNA RPE1       ATAGGCATGTGACAACTGCAGAGGCTCCTGGAACCACAGCTGGCCAAGTGCCTACTACAG 521
                ************************************************************

cDNA CH         AAGTCATGGGCACCACACCTGGCCAGGTGCCAACTGCAGAGGCCCCTGGCACCACAGTTG 1080
cDNA RPE1       AAGTCATGGGCACCACACCTGGCCAGGTGCCAACTGCAGAGGCCCCTGGCACCACAGTTG 581
                ************************************************************

cDNA CH         GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG 1140
cDNA RPE1       GGTGGGTGCCAACCACAGAGGATGTAGGTACCACACCTGAGCAGGTGGCAACCTCCAAAG 641
                ************************************************************

cDNA CH         TCTTAAGTACAACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG 1200
cDNA RPE1       TCTTAAGTACCACACCAGTGGAGATGCCAACTGCAAAAGCTACAGGTAGGACACCTGAAG 701
                ********** ***************************************************

cDNA CH         TGTCAACTACAGAGCCCTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGG 1260
cDNA RPE1       TGTCAACTACAGAGCCCTCTGGAACCACAGTTACACAGGGAACAACTCCAGAGCTGGTGG 761
                ************************************************************

cDNA CH         AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTCA 1320
cDNA RPE1       AGACCACAGCTGGAGAGGTGTCCACTCCTGAGCCTGCGGGTTCAAATACTAGCTCATTCA 821
                ************************************************************

cDNA CH         TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG 1380
cDNA RPE1       TGCCTACAGAAGGTACTGCAGGCTCCCTGAGTCCCCTGCCGGATGACACTGCCACCTTAG 881
                ************************************************************

cDNA CH         TCCTGGAGAAGCGCCAAGCCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC 1440
cDNA RPE1       TCCTGGAGAAGCGCCAAGCCCCCCTGGATTGTGTTCTGTATCGCTATGGCTCCTTTTCCC 941
                ************************************************************

cDNA CH         TCACCCTGGACATTGTCCAGGGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCA 1500
cDNA RPE1       TCACCCTGGACATTGTC---AGTATTGAGAGTGCTGAGATCCTACAGGCTGTGTCATCCA 998
                ***************    ***************************************

cDNA CH          GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT 1560
cDNA RPE1        GTGAAGGAGATGCATTTGAGCTGACTGTGTCTTGCCAAGGCGGGCTACCCAAGGAAGCCT 1058
                 ************************************************************

cDNA CH         GCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGC 1620
cDNA RPE1       GCATGGACATCTCATCGCCAGGGTGTCAGCTGCCTGCCCAGCGGCTGTGTCAGCCTGTGC 1118
                ************************************************************

cDNA CH         CCCCCAGCCCAGCCTGCCAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCT 1680
cDNA RPE1       CCCCCAGCCCAGCCTGCCAGCTGGTTTTGCACCAGGTACTGAAGGGTGGCTCAGGGACCT 1178
                ************************************************************

cDNA CH         ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG 1740
cDNA RPE1       ACTGCCTCAATGTGTCTTTGGCTGATGCCAATAGCCTGGCGATGGTCAGCACCCAGCTTG 1238
                ************************************************************

cDNA CH         TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCGTGGGCATCTTGCTGG 1800
cDNA RPE1       TCATGCCTGGGCAAGAAGCAGGCCTCAGGCAGGCTCCTCTGTTCGTGGGCATCTTGCTGG 1298
                ************************************************************

cDNA CH         TGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGCGAAGACTTATGAAGCAAGGCT 1860
cDNA RPE1       TGCTAACAGCTTTGTTGCTTGCATCTCTGATATACAGGCGAAGACTTATGAAGCAAGGCT 1358
                ************************************************************

cDNA CH         CAGCAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG 1920
cDNA RPE1       CAGAAGTCCCCCTTCCCCAGCTGCCACACGGTAGAACCCAGTGGCTACGTCTGCCCTGGG 1418
                *** ********************************************************
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Figure 3 (continued 1)

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cDNA CH         TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1980
cDNA RPE1       TCTTCCGCTCTTGCCCCATTGGTGAGAGCAAACCCCTCCTCAGTGGACAGCAGGTCTGAG 1478
                ************************************************************

cDNA CH         TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 2040
cDNA RPE1       TGCTCTTATGTGAAGTCATGATTTACCCAGGTGGACAGCAAGGCCTGTCTTTTCTCTGGT 1538
                ************************************************************
cDNA CH         CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 2086
cDNA RPE1       CTTCCCTCAGAGACTACCATTGCCTGAAATAAAGACTCAGAACTTG 1584
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Figure 3 (continued 2)

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Prot. CH        MDLVLRKYLLHVALMGVLLAVRTTEGPRDRDWLGVSRQLRIKAWNRQLYPEWTESQGPDC 60
Prot.RPE1       ------------------------------------------------------------

Prot.CH         WRGGHISLKVSNDGPTLIGANASFSIALHFPKSQKVLPDGQVIWANNTIINGSQVWGGQL 120
Prot.RPE1       ------------------------------------------------------------

Prot.CH         VYPQEPDDTCIFPDGEPCPSGPLSQKRCFVYVWKTWDQYWQVLGGPVSGLSIGTDKAMLG 180
Prot.RPE1       -----------------------------------QYWQVLGGPVSGLSIGTDKAMLG 23
                                                   ***********************

Prot.CH         TYNMEVTVYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF 240
Prot.RPE1       TYNMEVTVYHRRGSQSYVPLAHSSSAFTITDQVPFSVSVSQLQALDGRNKRFLRKQPLTF 83
                ************************************************************

Prot.CH         ALQLHDPSGYLAGADLSYTWDFGDSTGTLISRALTVTHTYLESGPVTAQVVLQAAIPLTS 300
Prot.RPE1       ALQLHDPSGYLAGADLSYTWDFGDSTGTLISRALTVTHTYLESGPVTAQVVLQAAIPLTS 143
                ************************************************************

Prot.CH         CGSSPVPGTTDRHVTTAEAPGTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG 360
Prot.RPE1       CGSSPVPGTTDRHVTTAEAPGTTAGQVPTTEVMGTTPGQVPTAEAPGTTVGWVPTTEDVG 203
                ************************************************************

Prot.CH         TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP 420
Prot.RPE1       TTPEQVATSKVLSTTPVEMPTAKATGRTPEVSTTEPSGTTVTQGTTPELVETTAGEVSTP 263
                ************************************************************

Prot.CH         EPAGSNTSSFMPTEGTAGSLSPLPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIVQGIE 480
Prot.RPE1       EPAGSNTSSFMPTEGTAGSLSPLPDDTATLVLEKRQAPLDCVLYRYGSFSLTLDIV-SIE 322
                ************************************************************ **

Prot.CH         SAEILQAVSSSEGDAFELTVSCQGGLPKEACMDISSPGCQLPAQRLCQPVPPSPACQLVL 540
Prot.RPE1       SAEILQAVSSSEGDAFELTVSCQGGLPKEACMDISSPGCQLPAQRLCQPVPPSPACQLVL 382
                ************************************************************

Prot.CH         HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAGLRQAPLFVGILLVLTALLLASL 600
Prot.RPE1       HQVLKGGSGTYCLNVSLADANSLAMVSTQLVMPGQEAGLRQAPLFVGILLVLTALLLASL 442
                ************************************************************

Prot.CH         IYRRRLMKQGSAVPLPQLPHGRTQWLRLPWVFRSCPIGESKPLLSGQQV 649
Prot.RPE1       IYRRRLMKQGSEVPLPQLPHGRTQWLRLPWVFRSCPIGESKPLLSGQQV 491
                *********** ***************************************
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Figure 4